

FT	DOMAIN	231	251	POTENTIAL.
FT	CANBOHD	45	45	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	NON_TER	595	595	
SO	SEQUENCE	595 AA;	66238 MM;	SDER30D649ACEB5BA CRC64;
Query Match 95.8%; Score 3093; DB 1; Length 595;				
Best Local Similarity 100.0%; Pred. No. 9.5e-216;				
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	MAMLRQLPSTAFSLFHFGLTPEVLFLNGLRAEAGSGSDVPSTQNNESGSSDCKEGVIL	60	
DB	1	MAMLRQLPSTAFSLFHFGLTPEVLFLNGLRAEAGSGSDVPSTQNNESGSSDCKEGVIL	60	
QY	61	PIWPEPNSLGDKIARVIVYFVALIYMFVGSIIADRFMASIEVITTSQREVTIKRPNGE	120	
DB	61	PIWPEPNSLGDKIARVIVYFVALIYMFVGSIIADRFMASIEVITTSQREVTIKRPNGE	120	
QY	121	TSTTIRWNEVNSULTLMAAGSSAPETLLSILEVCGHGFAGDGPSTIVGSAAPNNFI	180	
DB	121	TSTTIRWNEVNSULTLMAAGSSAPETLLSILEVCGHGFAGDGPSTIVGSAAPNNFI	180	
QY	181	IIGICVVIYPDGETRKIKHLRVFTTAAMSPATYIMLVIILAVFSPGVQVWEGLLTTFE	240	
DB	181	IIGICVVIYPDGETRKIKHLRVFTTAAMSPATYIMLVIILAVFSPGVQVWEGLLTTFE	240	
QY	241	FPVCVLLAVADVADRLLFYKYMHKRYRTDKHRCIIETEGDHKGIEMDGKMMNSHFLDGN	300	
DB	241	FPVCVLLAVADVADRLLFYKYMHKRYRTDKHRCIIETEGDHKGIEMDGKMMNSHFLDGN	300	
QY	301	LVPLEGKEVDESRRRMMIRLKDOKKHPEKDLDOLEVANAYALSHOOKSRAFYRIQATR	360	
DB	301	LVPLEGKEVDESRRRMMIRLKDOKKHPEKDLDOLEVANAYALSHOOKSRAFYRIQATR	360	
QY	361	MMTGAGNIIKKRAAEOAKKASMSGVHNDPEPDFISKYFPDPCSYQCLENGCAVLLTVVR	420	
DB	361	MMTGAGNIIKKRAAEOAKKASMSGVHNDPEPDFISKYFPDPCSYQCLENGCAVLLTVVR	420	
QY	421	KGDMKSMYVDYKTEDGSANAGADYEETEGTVVLKPGETOKESFVGIIIDDIPEDEHFE	480	
DB	421	KGDMKSMYVDYKTEDGSANAGADYEETEGTVVLKPGETOKESFVGIIIDDIPEDEHFE	480	
QY	481	FVRLSNVRIEEQPEEGHPAIFNSLPRLPRAVLASPCVATYIILDDDHAGITFECDITH	540	
DB	481	FVRLSNVRIEEQPEEGHPAIFNSLPRLPRAVLASPCVATYIILDDDHAGITFECDITH	540	
QY	541	VSESIGVNEVKLRTSGARGTYIVFPFVEGAKGGGDEPDTYGELEPKNDETY	595	
DB	541	VSESIGVNEVKLRTSGARGTYIVFPFVEGAKGGGDEPDTYGELEPKNDETY	595	
RESULT 2				
AC	NAC3_RAT	STANDARD:	PRT:	927 AA.
AC	P70549:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein			
DE	3)			
GN	SLC8A3 OR NCX3.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid:10116;			
RA	NCBI			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-Sprague-Dawley; TISSUE-Brain;			
RX	MEDLINE-96394663; PubMed-8798769;			
RA	Nicolli D.A., Quednau B.D., Qiu Z., Xia Y.-R., Lusis A.J.,			
RA	Phillipson K.D.;			
RT	"Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.";			
LT	J. Biol. Chem. 271:24914-24921(1996).			

CC	-1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC	-1- ENZYME REGULATION: BY INTRACELLULAR CALCIUM IONS.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- TISSUE SPECIFICITY: EXPRESSION RESTRICTED TO BRAIN AND SKELETAL MUSCLE.
CC	-----
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-slb.ch/announce/).
CC	or send an email to license@isb-slb.ch .
CC	-----
DR	EMBL: U53420: AAC52817.1: -
DR	InterPro: IPR003644; Calx_beta.
DR	InterPro: IPR004837; NaCa_Exmemb.
DR	InterPro: IPR004836; Na_Ca_Ex.
DR	Pfam: PF01699; Na_Ca_Ex; 2.
DR	Pfam: PF03160; Calx_beta; 2.
DR	PRINTS: PR01259; NACAEXCHNGR.
DR	SMART: SM00237; Calx_beta; 2.
DR	TIGRFAMs: TIGR00845; calca; 1.
RW	Transport: Antiport; Calcium
RW	Transmembrane; Glycoprotein; Phosphorylation; signal;
KV	Calmodulin-binding; Repeat.
KV	SIGNAL
FT	1 30
FT	CHAIN
FT	31 927
FT	DOMAIN
FT	31 73
FT	TRANSMEM
FT	74 94
FT	DOMAIN
FT	95 147
FT	TRANSMEM
FT	148 168
FT	DOMAIN
FT	169 169
FT	TRANSMEM
FT	170 190
FT	DOMAIN
FT	191 202
FT	TRANSMEM
FT	203 223
FT	DOMAIN
FT	224 230
FT	TRANSMEM
FT	231 251
FT	DOMAIN
FT	252 726
FT	TRANSMEM
FT	727 747
FT	DOMAIN
FT	748 754
FT	TRANSMEM
FT	755 775
FT	DOMAIN
FT	776 778
FT	TRANSMEM
FT	779 799
FT	DOMAIN
FT	800 828
FT	TRANSMEM
FT	829 849
FT	DOMAIN
FT	850 860
FT	TRANSMEM
FT	861 881
FT	DOMAIN
FT	882 903
FT	TRANSMEM
FT	904 924
FT	DOMAIN
FT	925 927
FT	DOMAIN
FT	253 272
FT	REPEAT
FT	140 180
FT	REPEAT
FT	399 470
FT	REPEAT
FT	534 604
FT	REPEAT
FT	796 832
FT	DOMAIN
FT	645 648
FT	CARBOHYD
FT	45 45
FT	CARBOHYD
FT	823 823
FT	SEQUENCE
SO	927 AA; 103162 MW; EAB35F9620DBE69E CRC64;
QY	Query Match
DB	Matches
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
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1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
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1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
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1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
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1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
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1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDVPTGONNESCSSGSSDCKEGYIL 60
1	MAWLRLOPLTSAFLHFGVTFVFLFNGLRRAENGSGSDV

ID	NAME	STANDARD	PRT	970 AA
Db	61	PIWPEPNSLDGDIARVIVYFVALYIMPLGVSIIADRMASELEVITTSDBREVTIKKPRGE	120	
Oy	121	TSITIRWNETVSNLTLMALGSSAPETILLSTIEVCGHGFIAGDGLSPSTIVGSAAFNMFI	180	
Db	121	TSTFTIRWNETVSNLTLMALGSSAPETILLSTIEVCGHGFIAGDGLSPSTIVGSAAFNMFI	180	
Oy	181	IIGTCVYVYIPGSEPTKKIKHLRVEFTTAMSSIFAYITWLTMLAVSPGYQWEGLLTFE	240	
Db	181	IIGTCVYVYIPGSEPTKKIKHLRVEFTTAMSSIFAYITWLTMLAVSPGYQWEGLLTFE	240	
Oy	241	FPVCVLLAMVADKRLLEFKYMHKKYRTQKHGIIIEETGSDHPKGIEMDGKMNSHFLDGN	300	
Db	241	FPVCVLLAMVADKRLLEFKYMHKKYRTQKHGIIIEETGSDHPKGIEMDGKMNSHFLDGN	300	
Oy	301	LVPLEGEKVEDSRREMIRILDKLKKHPEKDLQDQVEANANYALSHOOKSRAFYRIQATR	360	
Db	301	LVPLEGEKVEDSRREMIRILDKLKKHPEKDLQDQVEANANYALSHOOKSRAFYRIQATR	360	
Y	361	MMTGAGNLLKHAQAQAKKASSMSVHTDEPDEFTSKYFEDPCSTQCEENGCAVLLTVVR	420	
Db	361	MMTGAGNLLKHAQAQAKKASSMSVHTDEPDEFTSKYFEDPCSTQCEENGCAVLLTVVR	420	
Oy	421	KGDDSKTMYDYKTEKEDSANAAGAYEPTEGVYVLPKPEETOKESFVGIIIDDIPEDEHF	480	
Db	421	KGDDSKTMYDYKTEKEDSANAAGAYEPTEGVYVLPKPEETOKESFVGIIIDDIPEDEHF	480	
Oy	481	FVRLSNVRIIEEPEEGEPAPAFNSLP,PRAVLASPCATVYIILDDDHAGIFTFECDDTIH	540	
Db	481	FVRLSNVRIIEEPEEGEPAPAFNSLP,PRAVLASPCATVYIILDDDHAGIFTFECDDTIH	540	
Oy	541	VSESIGVEVKVYLRTSGARGTIVYFPRVEGTAKGGEDFEDTYGELEFKNDETV	595	
Db	541	VSESIGVEVKVYLRTSGARGTIVYFPRVEGTAKGGEDFEDTYGELEFKNDETV	595	
RESULT 3				
NACL_CANFA	NACL_CANFA	STANDARD	PRT	970 AA
AC	P23685			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).			
GN	SLC8A1.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_Taxid:9615;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Heart;			
RX	MEDLINE=91047958; PubMed=1785844;			
RA	Nicolli D.A., Longoni S., Philipson K.D.;			
RT	"Molecular cloning and functional expression of the cardiac sarcolemmal Na(+)-Ca2+ exchanger.";			
RL	Science 250:562-565(1990).			
RM	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Heart;			
RX	MEDLINE=92152737; PubMed=1785844;			
RA	Nicolli D.A., Philipson K.D.;			
RT	"Molecular studies of the cardiac sarcolemmal sodium-calcium exchanger.";			
RL	Ann. N.Y. Acad. Sci. 639:181-188(1991).			
CC	-1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION			
CC	COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION			
CC	SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.			
CC	-1- ENZYME REGULATION: BY ATP.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.			
CC	-1- TISSUE SPECIFICITY: CARDIAC SARCOLEMA.			
CC	THIS SWISS-PROT entry is copyright It is produced through a collaboration			

[illegible]

DB 117 GERTKTTRVIMNETVSNLTMLALGSSAPEILLSVIEVCGHNTAGDLPSTIVGSAAFNM 176
QY 179 FIITGICVYIPDGETRKHRLRVFTTAMSFAYITMLMTAVFSPGVVOVWEGLLT 238
DB 177 FIITACVYVPOGETRKHRLRVFTTAMSFAYITMLMTAVFSPGVVOVWEGLLT 236
QY 239 FEPVPCVLLAMVADKRLLFYKYMHHKYRTDKHNGIITETGDPHKG---TMDGKMMNSH 295
DB 237 FEPVICVFAVMDRLRLFYKYYKRYRACKQGMITEHGDGRSSKTEIEMDGKVVNSH 296
QY 296 ---FLOGNLVPLGEKVD---ESRREMITLIDKOKHPEKDLDOLEVANNTALSHQQ 348
DB 297 VDNFLGALV-LEVDREDOODEERARMARILKELKOKHPEKDLDOLEVANNTALSHQQ 355
QY 349 KSRAFYRIQATRMVGTAGNLIKKAPOAKASSMSEVHDEDE-DEISVFEFDPGSCYC 407
DB 356 KSRAFYRIQATRMVGTAGNLIKKAPOAKASSMSEVHDEDE-DEISVFEFDPGSCYC 415
QY 408 LENCAGVLLTVVRKGDMSKTMVYKTEDGSANAGADYETGTVVLRKPGTOKESVSG 467
DB 416 LENCAGVLLTVVRKGDMSKTMVYKTEDGSANAGADYETGTVVLRKPGTOKESVSG 475
QY 468 IIDDIFEEDEHFPVRLSNRIEEOPEECMPAIFNSLPLPAVYVLTITLDD 527
DB 476 IIDDIFEEDEHFPVRLSNRIEEOPEECMPAIFNSLPLPAVYVLTITLDD 532
QY 528 HAGIFEECTIVHSEISIGVMEYKVLRTSGARGTVIPEFTVGTAKGGEDFEDTGC 587
DB 533 HAGIFEECTIVHSEISIGVMEYKVLRTSGARGTVIPEFTVGTAKGGEDFEDTGC 592
QY 588 EFRNDETV 595
DB 593 EFRNDETV 600

RESULT 4
ID NACL_FELCA STANDARD: PRT: 970 AA.
AC P48767; P79174;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/calcium exchanger 1 precursor (Na⁺)/Ca²⁺-exchange protein 1).
GN SLC8A1 OR NCX1.
OS Fella silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxId=9685;
NN 11
NC SEQUENCE FROM N.A.
NC TISSUE=Heart;
RX MEDLINE=96250114; PubMed=8659865;
RA Menick D.R., Barnes K.V., Thacker U.F., Dawson M.M.,
RA McDermott D.E., Rozlich J.D., Kent R.L., Cooper G.;
RT "The exchanger and cardiac hypertrophy."
RL Ann. N.Y. Acad. Sci. 779:489-501(1996).
RN 12
RP SEQUENCE OF 1-600 FROM N.A.
RX MEDLINE=97269065; PubMed=9111065;
RA Barnes K.V., Cheng G., Dawson M.M., Menick D.R.;
RT "Cloning of cardiac, kidney, and brain promoters of the feline ncx1 gene."
RL J. Biol. Chem. 272:11510-11517(1997).
CC -1- FUNCTION: RAPIDLY TRANSPORTS CA²⁺ DURING EXCITATION-CONTRACTION COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -1- ENZYME REGULATION: BY ATP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC -1- TISSUE SPECIFICITY: CARDIAC SARCOLEMMMA.
CC -----
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CC -----
DR EMBL: L35846; AAB41941.1; -
DR EMBL: U67075; AAB40148.1; -
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Exmemb.
DR InterPro: IPR004836; NaCa_Ex.
DR Pfam: PF01699; Na_Ca_Ex; 2.
DR Pfam: PF03160; Calx_beta; 2.
DR PRINTS: PR01259; NACAEXCHNGR.
DR SMART: SM00237; Calx_beta; 2.
DR TIGRfams: TIGR00845; caca; 1.
KW transport; Sodium transport;
KW transport; Antiport; Calcium transport;
KW transmembrane; Glycoprotein;
KW Calmodulin-binding; Repeat.
FT SIGNAL 1 32
FT CHAIN 33 970
FT DOMAIN 33 71
FT TRANSMEM 72 93
FT DOMAIN 94 133
FT TRANSMEM 134 155
FT DOMAIN 156 167
FT TRANSMEM 168 188
FT DOMAIN 189 199
FT TRANSMEM 200 222
FT DOMAIN 223 225
FT TRANSMEM 226 249
FT DOMAIN 250 769
FT TRANSMEM 770 789
FT DOMAIN 790 796
FT TRANSMEM 797 819
FT TRANSMEM 820 821
FT TRANSMEM 822 840
FT DOMAIN 841 871
FT TRANSMEM 872 892
FT DOMAIN 893 903
FT TRANSMEM 904 924
FT DOMAIN 925 941
FT TRANSMEM 942 958
FT DOMAIN 959 970
FT TRANSMEM 971 178
FT DOMAIN 179 188
FT REPEAT 189 199
FT REPEAT 407 478
FT REPEAT 539 609
FT REPEAT 839 875
FT DOMAIN 889 929
FT DOMAIN 930 992
FT DOMAIN 993 1000
FT MOD_RES 389 389
FT CARBOHYD 41 41
FT CARBOHYD 157 157
FT CARBOHYD 21 21
FT CONFLICT 113 113
SQ SEQUENCE 970 AA; 108004 MW; 2402F02DE35D4057 CQC64;
Query Match 66.7%; Score 2152.5; DB 1; Length 970;
Best Local Similarity 70.0%; Pred. No. 1,5e-147;
Matches 426; Conservative 72; Mismatches 88; Indels 23; Gaps 10;
QY 1 MAHLRIQPLTSATLHFGVLFV-LFLNGLAELAGSGDVPSTGONNES--CSGSSCKEG 57
DB 1 MLRLSPFVSFGVH-LAFLVPLFSVHDL---SADVEMEGGNTGECTSYCKKG 55
QY 58 VILPIWPNPSSLDGIARIYVYFVALIYFGLSVIADRFMAISIEVTSQREVTYIKRP 117
DB 56 VILPIWPNPSSLDGIARIYVYFVALIYFGLSVIADRFMAISIEVTSQREVTYIKRP 115
QY 118 NGSTSTTRVIMNETVSNLTMLALGSSAPEILLSVIEVCGHNTAGDLPSTIVGSAAFNM 177

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Db 116 NGETTAKTVARINNEFVSNULTLMLAGSSAPELLISVIEVCGHNFTAGLDGSTIVGSAFN 175
Oy 178 MFIITIGCVIYIPDGETRKKIHLNRFVFTTAAMSIFAYITLMLAVSPGVQVMEGLT 237
Db 176 MFIITALCVVYVDPGETRKIKHLRFVFTTAAMSIFAYITLMLAVSPGVQVMEGLT 235
Oy 238 LEFPVVCVLLAVMDKRLLEFYKYMHHKKYRDKKHGIIITEBGHPKC--IEMDGKMN 234
Db 236 FEFPEPICVAFVMDRLLLFYKYKYKRRRAKQKGMTEIEHGDBRSSKTEIEMDGKVN 295
Oy 295 H---FLDNLNLPLEGEKVD---ESRREMRITLKDLOKHPKLDQVEMANYALSHQ 347
Db 296 HDVNFLDGALV-LEVDERDQDDEGARREMARILKELQKHPKEIEBLIETLANQVLSQ 354
Oy 348 QKSRAFYRIQATRWMTGAGNLIKHLAAEQAKASSMSEVHTDEP-DFIKVEFDPSCYQ 406
Db 355 QKSRAFYRIQATRWMTGAGNLIKHLAAEQAKASSMSEVHTDEP-DFIKVEFDPSCYQ 414
Oy 407 CLENGAVLLTVKRGKGMSTMYVYKTEDEGSANAGADIEFTGTVLVRPEFOKEFSY 466
Db 415 CLENGVTAALLIRKGGDLNTVPEVDERTEGTINAGSDIEFTGTVLVRPEFOKEIRV 474
Oy 467 GIIDDIDEEDEHFFVRISNVRIEEDPEEGEMPAFENSILPLRAVLAISCVATVTLDD 526
Db 475 GIIDDIDEEDEENFLVHLSNKKVSSASESDILEANVNS--TLACGSPSTAVTITFDD 531
Oy 527 DHAGIFTECDTHVSESIGVMEYKVLRTSGARCTVIVPFTVEGTAKGGEDEFEDTGE 586
Db 532 DHAGIFTEEPVTHVSESIGVMEYKVLRTSGARCNVIVPRTTIGTARGGGEDEFEDTGE 591
Oy 587 LEFKNDENV 595
Db 592 LEFONDEIV 600

RESULT 5
NACL_BOVIN STANDARD; PRT: 970 AA.
AC P48765;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).
GN SLC8A1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bovinae; Bos.
OC NCBI_taxid=9913;
OX (1)
RN SEQUENCE FROM N.A.
RP TISSUE-Heart.
RC MEDLINE=93037494; Pubmed=1416984.
RX Accio J.F., Condrescu M., Kroupis C., Nelson H., Nelson N., Nicol D.A., Phillips K.D., Reeves J.P.;
RT "Cloning and expression of the bovine cardiac sodium-calcium exchanger."
RT Arch. Biochem. Biophys. 298:553-560(1992).
RL (2)
RN SUBCELLULAR LOCATION.
RC TISSUE-Retinal rod cell;
RX MEDLINE=90241959; Pubmed=2334719;
RA Reid D.M., Friedel U., Molday R.S., Cook N.J.;
RT "Identification of the sodium-calcium exchanger as the major rizin-binding glycoprotein of bovine rod outer segments and its localization to the plasma membrane."
RL Biochemistry 29:1601-1607(1990).
CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION COUPLING. CA(2+) IS EXTRUDED OUT OF THE CELL DURING RELAXATION SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -1- ENZYME REGULATION: By ATP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.

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CC	-1	TISSUE SPECIFICITY: CARDIAC SARCOLEMA.
CC	CC	-----
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	CC	use by non-profit institutions as long as its content is in no way
CC	CC	modified and this statement is not removed. Usage by and for commercial
CC	CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC	CC	or send an email to license@isb-sib.ch).
CC	CC	-----
DR	DR	EMBL: L06438; AAA30509.1; -.
DR	DR	InterPro: IPR003644; Calx_beta.
DR	DR	InterPro: IPR004837; NaCa_Exemb.
DR	DR	InterPro: IPR004836; Na_Ca_Ex.
DR	DR	Pfam: PF01699; Na_Ca_Ex; 2.
DR	DR	Pfam: PF03160; Calx_beta; 2.
DR	DR	PRINTS: PR01259; NACAEXCHNR.
DR	DR	SMART: SM00237; Calx_beta; 2.
DR	DR	TIGRFAMs: TIGR00845; caca; 1.
RW	RW	Transport; Antiport; Calcium
KW	KW	Transmembrane; Glycoprotein; Phosphorylation; signal;
KM	KM	Calmodulin-binding; Repeat.
FT	FT	SIGNAL 1 32 POTENTIAL.
FT	FT	CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	FT	DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
FT	FT	DOMAIN 72 93 POTENTIAL.
FT	FT	DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
FT	FT	TRANSMEM 134 155 POTENTIAL.
FT	FT	DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).
FT	FT	TRANSMEM 168 188 POTENTIAL.
FT	FT	DOMAIN 189 199 CYTOPLASMIC (POTENTIAL).
FT	FT	TRANSMEM 200 222 POTENTIAL.
FT	FT	DOMAIN 223 225 EXTRACELLULAR (POTENTIAL).
FT	FT	TRANSMEM 226 249 POTENTIAL.
FT	FT	DOMAIN 250 769 CYTOPLASMIC (POTENTIAL).
FT	FT	TRANSMEM 770 789 POTENTIAL.
FT	FT	DOMAIN 790 796 EXTRACELLULAR (POTENTIAL).
FT	FT	TRANSMEM 797 819 POTENTIAL.
FT	FT	DOMAIN 820 821 CYTOPLASMIC (POTENTIAL).
FT	FT	TRANSMEM 822 840 POTENTIAL.
FT	FT	DOMAIN 841 871 EXTRACELLULAR (POTENTIAL).
FT	FT	TRANSMEM 872 892 POTENTIAL.
FT	FT	DOMAIN 893 903 CYTOPLASMIC (POTENTIAL).
FT	FT	TRANSMEM 904 924 POTENTIAL.
FT	FT	DOMAIN 925 941 EXTRACELLULAR (POTENTIAL).
FT	FT	TRANSMEM 942 958 POTENTIAL.
FT	FT	DOMAIN 959 970 CYTOPLASMIC (POTENTIAL).
FT	FT	TRANSMEM 970 970 CALMODULIN-BINDING (POTENTIAL).
FT	FT	DOMAIN 251 270 ALPHA-1.
FT	FT	TRANSMEM 271 278 POTENTIAL.
FT	FT	DOMAIN 279 286 BETA-1.
FT	FT	TRANSMEM 287 294 BETA-2.
FT	FT	DOMAIN 295 302 ALPHA-2.
FT	FT	TRANSMEM 303 310 POLY-PHE.
FT	FT	DOMAIN 311 318 POLY-GLU.
FT	FT	TRANSMEM 319 326 POLY-ASP.
FT	FT	DOMAIN 327 334 PHOSPHORYLATION (POTENTIAL).
FT	FT	TRANSMEM 335 342 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 343 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 351 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 359 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 367 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 375 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 383 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 391 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 399 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 407 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 415 422 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 423 430 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 431 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 439 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 447 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 455 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 463 470 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 471 478 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 479 486 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 487 494 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 495 502 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 503 510 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 511 518 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 519 526 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 527 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 535 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 543 550 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 551 558 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 559 566 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 567 574 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 575 582 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 583 590 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 591 598 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 599 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 607 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 615 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 623 630 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	DOMAIN 631 638 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	TRANSMEM 639 646 N-LINKED (GLCNAC. . .) (POTENTIAL

FT	DOMAIN	254	973	CYTOPLASMIC (POTENTIAL) .
FT	DOMAIN	252	273	CALMODULIN-BINDING (POTENTIAL) .
FT	REPEAT	141	181	ALPHA-1 .
FT	REPEAT	410	481	BETA-1 .
FT	REPEAT	542	612	BETA-2 .
FT	REPEAT	842	878	ALPHA-2 .
FT	DOMAIN	239	242	POLY-PHE .
FT	DOMAIN	692	695	POLY-GLU .
FT	DOMAIN	759	763	POLY-ASP .
FT	MOD_RES	392	392	PHOSPHORYLATION (POTENTIAL) .
FT	CARBOHYD	44	44	N-LINKED (GLCNAC . . .) (POTENTIAL) .
FT	CARBOHYD	160	160	N-LINKED (GLCNAC . . .) (POTENTIAL) .
FT	CARBOHYD	869	869	N-LINKED (GLCNAC . . .) (POTENTIAL) .
FT	VARSPLIC	605	613	TISKAVID > ITTITIEDR (IN ISOFORM 3 ,
FT				ISOFORM 7 AND ISOFORM 10) .
FT	VARSPLIC	619	645	NKTFELEGEBRLVEMSEKALLNEL -> ECSFSYLEE
FT				PKWIRGMR (IN ISOFORM 3 , ISOFORM 7 AND
FT				ISOFORM 10) .
FT	VARSPLIC	652	656	MISSING (IN ISOFORM 7) .
FT	VARSPLIC	652	679	MISSING (IN ISOFORM 3) .
SO	SEQUENCE	973 AA; 108546 MW; 17DFC1B1F15921D8 CRC64;		
Query Match				
Best Local Similarity 66.5%; Score 2146.5; DB 1; Length 973;				
Matches 421; Conservative 76; Mismatches 90; Indels 21; Gaps				
OY	1	MAMRLQPLTSAFLHFGVLTFLV--LNGLRADAGSGDVPSTGQNNESCGSSDDCKEGV	58	
Db	4	MKRLSLSPFSGMFLHVLTVSLFSGHVHVIATIEGEGENETGE---CTGSSYCKKGV	59	
OY	59	ILPIWYRPNPSPGDKIARIYIVFVLLIYWLGLVSTIADRFMSIEYTSOEBEYTKRPN	118	
Db	60	ILPIWEPDPSGDKIARTYIVFVMMVYLFVSTIADRFMSIEYTSQEKETTKRPN	119	
OY	119	GETSTTRVWNETYSNLTLMALGSSAPILLSLIEVCGHGTIAGDIPSTIVGSAFNM	178	
Db	120	GETTQTVYRINMETYSNLTLMALGSSAPILLSLIEVCGHNTIAGDIPSTIVGSAFNM	179	
OY	179	FIIGICVYVIRPDGERTKIKILRVFFITFAMGIFAVILWMLIAFVSPGVQVMEGLTL	238	
Db	180	FIILMCAVYVDPDGETRKIKILRVFFVFMAGSIFAVTWLIILSVISPGVVEWEGLLTF	239	
OY	239	FFEPVCVLLAWADKRLLFYKYMHKKRYRDKRGITIEEGDHPKC---IEMDGKMMNH	295	
Db	240	FFEPICVVFAMVADKRLLFYKTYVRYKRGKQGMITEHGGDPPSSKTEIENDGKVNSH	299	
OY	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDKQKPEKLDQVLVMANYALSHOO	348	
Db	300	VENFLDGLALV-LEVDERODDDEARREMARILKELKQKPKDEIDELITLANTOYVLSOO	358	
OY	349	KSRAFYRIQATRMATGAGNIIKHAAEQAKKASSMSEVHTDPE-DFISKVFEDPCSYOC	407	
Db	359	KSRAFYRIQATRLMAGAGNIIKRNAADQARKAVSMHEVNT EYLTENDPVSCKIFEEQGTYC	418	
OY	408	LENCAGVLLTVYRKGDMSKTMVVDYKTTDGSANAGADLEFPEGTVYVLRPGEQKFSVG	467	
Db	419	LENGCTVALTLIIRGGDLNTVFVPRFEDGTANAGSDEFEETGVVFRPGTQKXIRVG	478	
OY	468	IIDDDIFEEDEHFRLSNVRIIEEDQPEEGMPATFNSJPLPRAVLASCAVATVTTDLD	527	
Db	479	IIDDDIFEEDEHFVHLNSVKKVSSSEKSESGILEANHV---FLACGSPSTATVTTTFDD	535	
OY	528	HAGIFTFECDTIIVSSESIGVMEVKVLRISGARGVYIVPRVEGTAKGGEDEFEEDTYGEL	587	
Db	536	HAGITTFEPRVTHVSESIGIMEVKVLRISGARGVYIVPYKTIEGTARGGGEDEPDTCGEL	595	
OY	588	EKKNDENV 595		
Db	596	EKONDEIV 603		

ID	NAME	STANDARD	PROT	AA
AC	PA4766;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).			
GN	SLC8A1.			
OS	Cavia porcellus (Guinea pig).			
OC	Eukaryota; Metazoa; Chordata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.			
OX	NCBI_TaxID:10141;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Heart;			
RX	MEDLINE-950789257; PubMed-7986817;			
RA	Tsuruya Y., Bersohn M.M., Li Z., Nicoll D.A., Phillips K.D.;			
RT	"Molecular cloning and functional expression of the guinea pig			
RL	cardiac Na(+)-Ca2+ exchanger.";			
CC	Biochem. Biophys. Acta 1196:97-99(1994).			
CC	-1 FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION			
CC	COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION			
CC	SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.			
CC	-1 ENZYME REGULATION: BY ATP.			
CC	-1 SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.			
CC	-1 TISSUE SPECIFICITY: CARDIAC SARCOLEMA.			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb.slb.ch/announce/or_send_an_email_to_license@isb.slb.ch).			
CC	-----			
DR	EMBL; U04955; AAA73904.1; ?;			
DR	InterPro; IPR003644; Calx_beta.			
DR	InterPro; IPR004837; NaCa_Extmb.			
DR	InterPro; IPR004836; Na_Ca_Ex.			
DR	Pfam; PF01699; Na_Ca_Ex; 2.			
DR	Pfam; PF03160; Calx_beta; 2.			
DR	PRINTS; PR01259; NACAECHNGR.			
DR	SMART; SM00237; Calx_beta; 2.			
DR	TIGRFAMs; TIGR00845; caca; 1.			
RW	transport; Antiport; Calcium			
KW	transmembrane; Glycoprotein;			
KW	Calmodulin-binding; Repeat.			
FT	SIGNAL	1	32	POTENTIAL.
FT	CHAIN	33	970	SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN	33	71	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	72	93	POTENTIAL.
FT	DOMAIN	94	133	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	134	155	POTENTIAL.
FT	DOMAIN	156	167	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	168	188	POTENTIAL.
FT	DOMAIN	189	199	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	200	222	POTENTIAL.
FT	DOMAIN	223	225	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	226	249	POTENTIAL.
FT	DOMAIN	250	769	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	770	789	POTENTIAL.
FT	DOMAIN	790	796	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	797	819	POTENTIAL.
FT	DOMAIN	820	821	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	822	840	POTENTIAL.
FT	DOMAIN	841	871	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	872	892	POTENTIAL.
FT	DOMAIN	893	903	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	904	924	POTENTIAL.
FT	DOMAIN	925	941	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	942	958	POTENTIAL.
FT	DOMAIN	959	970	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	970	970	POTENTIAL.
FT	DOMAIN	251	270	CALMODULIN-BINDING (POTENTIAL).

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FT REPEAT 138 178 ALPHA-1.
FT REPEAT 407 478 BETA-1.
FT REPEAT 539 609 BETA-2.
FT REPEAT 839 875 ALPHA-2.
FT DOMAIN 236 239 POLY-PHE.
FT DOMAIN 689 692 POLY-GLU.
FT DOMAIN 756 760 POLY-ASP.
FT MOD.RES 389 389 PHOSPHORYLATION (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 866 866 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 970 AA; 108071 MW; 720364C8BD157739 CnC64;

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Query Match 66.4%; Score 2142.5; DB 1; Length 970;
Best Local Similarity 69.1%; Pred. No. 7.9e-147;
Matches 420; Conservative 76; Mismatches 91; Indels 21; Gaps 9;

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OY 1 MAWLRLQPLTSARLH-FGLVTPVL-FLNGRAEAGSGDVPSTGQNNSSGSSDCKEY 58
DB 1 MLRLSPPTYSGLCFHLLAMTTLTSHVDHTAET---EKVEBNETGECTGSYKKG 56
OY 59 ILPIWYPPNSLDGKTAIVYVFEVALIYMEFGVSIADRFMAISIEYTSQREVTIKRP 118
DB 57 ILPIWYPPNSLDGKTAIVYVFEVALIYMEFGVSIADRFMAISIEYTSQREVTIKRP 116
OY 119 GETSTTIRVWNETVSNLTLMALGSSAPELLISLIEVCGHGTAGDLGPGSTIVGSAFNN 178
DB 117 GETTKTIVRWNETVSNLTLMALGSSAPELLISLIEVCGHGTAGDLGPGSTIVGSAFNN 176
OY 179 FIITIGCVVPIPDGETRKKIKHLVFEFITAAMSFAYIMLILAVSPGVVWVWELLTL 238
DB 177 FIITIGCVVPIPDGETRKKIKHLVFEFITAAMSFAYIMLILAVSPGVVWVWELLTL 236
OY 239 FEPPVCLLAWADKRLRYFYKMHKKYRTDKHNGIITETGDPKCG---IEMDKMMNSH 295
DB 237 FEPPICVFAWVADRRLRFYKYYKRYRAGKQGMIIIEHGDPSKTELEMGKAYVNSH 296
OY 296 ---FLDGNLVPLEGKEVD---ESREMRILKDLKQKPEKDLQVEMANTYALSHQ 348
DB 297 VENFDLGAIV-LEVDERDDDEAREMARIKELKQKPEKIEOLIELANQVLSQO 355
OY 349 KSRAPRIQATRMGTAGNLIKKAHAEQKAKSSMEVHTDEPE-DEISVFEFDPSCYC 407
DB 356 KSRAPRIQATRMGTAGNLIKKAHAEQKAKSSMEVHTDEPE-DEISVFEFDPSCYC 415
OY 408 LENCAGVALLTVKAGGDMSTMYDYKTEGDSANAGADYEFTEGTVLKPGETQKEFSVG 467
DB 416 LENCAGVALLTVKAGGDMSTMYDYKTEGDSANAGADYEFTEGTVLKPGETQKEFSVG 475
OY 468 IIDDIDFEDEHFFVLSNVRIEEOPEEGMPPAIRNSLPLPAVLASPCVATVTLLDD 527
DB 476 IIDDIDFEDEHFFVLSNVRIEEOPEEGMPPAIRNSLPLPAVLASPCVATVTLLDD 532
OY 528 HAGIFPEECDTIVSESGVMEYKVLRTSGARGTVPRTVETGKGGGEDEEDTYGEL 587
DB 533 HAGIFPEECDTIVSESGVMEYKVLRTSGARGTVPRTVETGKGGGEDEEDTYGEL 592
OY 588 EFKNDETV 595
DB 593 EFKNDETV 600

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA MEDLINE=93138118; PubMed=8422940;
RT Low W., Kasir J., Rahamimoff H.;
RT "Cloning of the rat heart Na(+)-Ca2+ exchanger and its functional
RL expression in HeLa cells.";
RL FEBS Lett. 316:63-67(1993).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RA MEDLINE=93202244; PubMed=8454039;
RT Furlan I., Cook O., Kasir J., Rahamimoff H.;
RT "Cloning of two isoforms of the rat brain Na(+)-Ca2+ exchanger gene
RL and their functional expression in HeLa cells.";
RL FEBS Lett. 319:105-109(1993).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney cortex;
RA MEDLINE=94253030; PubMed=8195112;
RT Lee S.-L., Yu A.S.L., Lytton J.;
RT "Tissue-specific expression of Na(+)-Ca2+ exchanger isoforms.";
RL J. Biol. Chem. 269:14849-14852(1994).
RN [4]
RP TISSUE SPECIFICITY.
RC STRAIN=Sprague-Dawley;
RA MEDLINE=96394663; PubMed=8798769;
RT Nicoll D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
RT Phillipson K.D.;
RT "Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.";
RL J. Biol. Chem. 271:24914-24921(1996).
CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
CC COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
CC SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -1- ENZYME REGULATION: BY ATP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC -1- ALTERNATIVE PRODUCTS: 5 isoforms; heart/NCX1 (shown here),
CC brain 1/NCX5, brain 2/NCX4, kidney 1/NCX7 and kidney 2/NCX3;
CC are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: CARDIAC SARCOLEMA OR BRAIN, AND SPLEEN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X68191; CAA48273.1; -
DR EMBL: X68812; CAA48707.1; -
DR EMBL: X68813; CAA48708.1; -
DR EMBL: U04933; AAB39952.1; -
DR EMBL: U04934; AAA19124.1; -
DR EMBL: U04936; AAA19125.1; -
DR PIR: S25552; S25552.
DR PIR: S28833; S28833.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Exmemb.
DR InterPro: IPR004836; NaCa_Ex.
DR Pfam: PF01699; NaCa_Ex; 2.
DR Pfam: PF03160; Calx_beta; 2.
DR PRINTS: PR01259; NACAEXCHNR.
DR SMART: SM00237; Calx_beta; 2.
DR TIGRfams: TIGR00845; caca; 1.
DR transport; Anticport; Calcium transport; Sodium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW Calmodulin-binding; Repeat; Alternative splicing.
FT SIGNAL 1 32
FT CHAIN 33 971 SODIUM/CALCIUM EXCHANGER 1.

```


[illegible]

Query Match	66.2%	Score 2135.5	DB 1	Length 971
Best Local Similarity	68.8%	Pred. No. 2.5e146		
Matches 421	Conservative 72	Mismatches 86	Indels 33	Gaps 9
OY	4	LRLQPLTSAFLHFGLVTFVLF-----NGLRAEAGSGSDPSTGONNESCSSGSDCK	55	
Db	2	LRLSLPPNVSWMGFRLLTVALLLFTVHVDHTTADTTEATGDN-----ETTECTGYYKK	53	
OY	56	EGVILPIWPPNPBSLGDKIARIYVFVALIYFLEVSIADNFPMASIEYITSOERVYTK	115	
Db	54	KGVIPIPIEPPOPSGDKIARATYFVAMVYFLEVSIADNFPMASIEYITSOEKRIYTK	113	
OY	116	KPNGETSTTIRVMNETHVSNLFLMALGSSAPRLLSLIEVCGHGTAGLDGSTIYGSNA	175	
Db	114	KPNGETTKTYVAINMETVSNLFLMALGSSAPRLLSLIEVCGHNTAGLDGSTIYGSNA	173	
OY	176	FNMETIIIGICVYVDPGETRIKILRVETITAMSIIPAYIMLMLAVFSPGVOWMEGL	235	
Db	174	FNMETIIICVYVDPGETRIKILRVFETVTAAMSIIPAYITWYIILSVSSPVEVMEGL	233	
OY	236	LTLFFEPVCVLLAWADRRLFLFYKIMHKYRFDKRGITIIETEGDHPK---IENDGKMM	292	
Db	234	LTLFFEPVCVFAWADRRLFLFYKIVKRYRKGKGMITIEHGDPRPASTETIENDGKVV	293	

Oy	293	NSH -FLDGNLVPLEGKVEVD-----ESRKMIRIILKDKOKHPKEDLPQVEMANYALSL
Dd	294	NSHDNFIIDGLALY-LEVDERRDDDEARERMARIIKEIKQHPPKEISOLIETLANYOVLSS
Oy	346	HQOKSRATFYRIQATPMYMGAGNIILKKHAAEQAOKKASSSEVHTDEPE-DFTSKVFDPDCS
Dd	353	QOQKSRAATYRIQATPLMTGAGNIILKRHAADQARKAVSHNEVMNDVENDPVSKEYFEEGCT
Oy	405	YQCENCGAVLLTVYRKRGDSKTMVVDYKTEDGSANAGADEFTEGTGVLLKPGETOKEF
Dd	413	YQCLENCTVALTLTIIRRGCDLTNTVFVDFPRTEDGTANAGSDYEFEFGTGVFKPGETOKEI
Oy	465	SVGIITDDIFEDDEFHFRLSNVRREEQPREGMPTAFNSLPLPR-AVLASPCATVTI
Dd	473	RGIITDDIFEDDEFENELVHLNSNRASSEVEDG----ILDSNHVASAIICLSPNTATTITI
Oy	524	LDDDHAGIFTEFCEDTHIVESIGVMEVNVLRTPSGARGTVIIVPRTVEGTAKGGGEDEDT
Dd	529	FDDDHAGIFTEFEPEPTYHSESIGIMEVAVLWRTSGARGVVIIPKYTIESTANGGGEDEDT
Oy	584	YGEELEKNDETV
Dd	589	CGELEFONDEIV
<p>RESULT 9</p>		
ID	NACL_MOUSE	STANDARD; PRT; 970 AA.
AC	P70414:	
DT	01-NOV-1997 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
De	Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein	
De	1).	
GN	SLC8A1 OR NCX.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_Taxid=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6;	
RX	MEDLINE=96250070; Pubmed=8659820;	
RA	Kim I., Lee C.O.;	
RT	"Cloning of the mouse cardiac Na(+)-Ca2+ exchanger and functional	
RL	expression in Xenopus oocytes."	
CC	Ann. N.Y. Acad. Sci. 779:126-128,(1996).	
CC	-I- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION	
CC	COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION	
CC	SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.	
CC	-I- ENZYME REGULATION: BY ATP.	
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.	
CC	-I- TISSUE SPECIFICITY: CARDIAC SARCOLEMMA.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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CC	use by non-profit institutions as long as its content is in no way	
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL: U70033; AAB46708.1; -.	
DR	MGP: MGI:107956; Slc8a1.	
DR	InterPro: IPR003644; Calx_beta.	
DR	InterPro: IPR004837; NaCa_Exmemb.	
DR	InterPro: IPR004836; Na_Ca_Ex.	
DR	pfam: PF01699; Na_Ca_Ex. 2.	
DR	pfam: PF03160; calx-beta; 2.	
DR	PRINTS: PR01259; NACAEXCHNR.	
DR	SMART: SM00237; Calx_beta; 2.	
DR	TIGRFAMs: TIGR00845; caca; 1.	
KW	Transport; Antiport; Calcium transport; Sodium transport;	


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FT DOMAIN 91 130 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 131 152 POTENTIAL.
FT DOMAIN 153 164 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 165 185 POTENTIAL.
FT DOMAIN 186 196 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 197 219 POTENTIAL.
FT DOMAIN 220 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 246 POTENTIAL.
FT DOMAIN 247 720 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 721 740 POTENTIAL.
FT DOMAIN 741 747 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 748 770 POTENTIAL.
FT DOMAIN 771 772 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 773 791 POTENTIAL.
FT DOMAIN 792 822 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 823 843 POTENTIAL.
FT DOMAIN 844 854 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 855 875 POTENTIAL.
FT DOMAIN 876 892 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 893 909 POTENTIAL.
FT DOMAIN 910 921 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 921 921 CALMODULIN-BINDING (BT SIMILARITY).
FT DOMAIN 248 267 POTENTIAL.
FT REPEAT 135 175 ALPHA-1.
FT REPEAT 397 468 BETA-1.
FT REPEAT 527 597 BETA-2.
FT REPEAT 790 826 ALPHA-2.
FT DOMAIN 29 32 POLY-PRO.
FT DOMAIN 638 641 POLY-GLU.
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 817 817 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 921 AA: 100367 MW: 798CDFE32B9410C CRC64:

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Query Match 60.7%: Score 1961; DB 1; Length 921;
 Best Local Similarity 65.7%: Pred. No. 9,3e-134;
 Matches 371: Conservative 87; Mismatches 83; Indels 24; Gaps 6;

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OY 40 STGNQNNSSGSDCKEGYILPIWPNPNSLDKTIARIVYFVALYMLGYIADRM 99
DB 39 STG-----CGGSSYRCQPGVLLPWERPDSDCKAKARAVYVAAWYMLGSIIDRM 94
OY 100 ASIEVITSOEREVYTKKPNGETSTTTIRVNETVSNLTMLAGSSAPEILLIEVCGHG 159
DB 95 AAIEVITSEKEITITKANGETSNGTVRIMNETVSNLTMLAGSSAPEILLIEVCGHN 154
OY 160 FLAGLGPSTIYGAFAFNFIIGICVYIPDGERKTHLNVFTTANSPFIATMLM 219
b 155 PAGELGPGTIVGAFAFNFIIVACITVYPAGESKRIKHLRFVFTASMSIFAYWML 214
OY 220 ILAVESPGVQVWEGLLTLFFPPCVLLAMVADKRLLEFKYMHKKRYTKHNGIITETG 279
DB 215 ILAVESPGVQVWEGLLTLFFPPCVLLAMVADKRLLEFKYMHKKRYTKHNGIITETG 274
OY 280 DHPKGIENDGKMMNSHFLDGNL-----VPLEKEVDESREMIKILDKQNHPEKDLDO 334
DB 275 DEPKSIELDGTFTVGAE-ARGELGGLGAPAEARELDASREYIQLIKDKQNHPEKDLDO 333
OY 335 LVEMANNYALSHQKSRATYRQATRMNTGAGNIIKHAADAKKASSSEVHTDEPEP 394
DB 334 LVGINNYALLHQKSRATYRQATRMNTGAGNIIKHAADAKKASSSEVHTDEPEP 392
OY 395 ISKVFEDPCSYOCLENCGAVLLTVYRKGDMSKTMVYDKTDEGSAAGADVEFTGTAV 454
DB 393 ASRIFFEPSTLYHCLNCGSVLLSYTCGSGEGNSTFTVYRTDEGSAKASDVEISGTLV 452
OY 455 LKPGETQKEFSVGIIDDDIFEEDEHFEVRLSNVRIEEG-----PEEGMPALFNSLPLDR 510
DB 453 FKPGETQKELRIGIIDDIFEEDEHFEVRLSNVRIEEG-----PEEGMPALFNSLPLDR 503
OY 511 AVLASPCVATVTIILDDHAGITFEEDTTHSESGVMKVLKRLSGANGTYIVPRTYE 570
DB 504 GRLVAPLLATVTIILDDHAGITFEEDTTHSESGVMKVLKRLSGANGTYIVPRTYE 563
OY 571 GTAKGGEDFEDTYGELFEKNDETV 595

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DB 564 GTARGGVHYHEDACGELFEKDDETM 588
||||| :|| :||| :|||
RESULT 11
ID NAC2_RAT STANDARD: PRT: 921 AA.
AC P48768:
DT 01-FEB-1996 (rel. 33, Created)
DT 01-FEB-1996 (rel. 33, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein
DE 2).
GN SLC8A2 OR NCX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE-Brain stem;
RX MEDLINE-94292496; PubMed-8021246;
RA Li Z., Matsuo S., Hryshko L.V., Nicoll D.A., Bersohn M.M.,
RA Burke E.P., Lifton R.P., Philipson K.D.;
RT "Cloning of the NCX2 isoform of the plasma membrane Na(+)-Ca2+
RT exchanger.";
RL J. Biol. Chem. 269:17434-17439(1994).
RN [2]
RP TISSUE SPECIFICITY.
RC STRAIN-Sprague-Dawley;
RX MEDLINE-96394663; PubMed-8798769;
RA Nicoll D.A., Quedzu B.D., Qui Z., Xia Y.-R., Lusis A.J.,
RA Philipson K.D.;
RT "Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.";
RL J. Biol. Chem. 271:24914-24921(1996).
CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
CC COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
CC SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -1- ENZYME REGULATION: BY ATP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN AND SKELETAL MUSCLE.
CC -----
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CC -----
DR EMBL: U08141; AAA19920.1; -
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Exmemb.
DR Pfam: PF01699; Na_Ca_Ex: 2.
DR Pfam: PF03160; Calx_beta: 2.
DR PRINTS: PR01259; NACAEXCHNGR.
DR SMART: SM00237; Calx_beta: 2.
DR TIGRFAMs: TIGR00845; caca; 1.
DR Transport: Antiport; Calcium transport; Sodium transport;
DR Transmembrane: Glycoprotein; Phosphorylation; signal;
KW Calmodulin-binding; Repeat.
FT SIGNAL 1 20
FT CHAIN 21 921
FT DOMAIN 21 68 SODIUM/CALCIUM EXCHANGER 2.
FT TRANSMEM 69 90 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 91 130 POTENTIAL.
FT TRANSMEM 131 152 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 153 164 POTENTIAL.
FT TRANSMEM 165 185 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 186 196 POTENTIAL.
FT TRANSMEM 197 219 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 220 222 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 605 625 POTENTIAL.
 FT DOMAIN 626 632 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 633 653 POTENTIAL.
 FT DOMAIN 654 663 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 170 210 ALPHA-1.
 FT REPEAT 543 574 ALPHA-2.
 FT MOD_RES 337 337 PHOSPHORYLATION (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 663 AA; 73771 MW; DD624E3080C43082 CRC64;

Query Match 6.5%; Score 209.5; DB 1: Length 663;
 Best Local Similarity 21.9%; Pred. No. 1.7e-07;
 Matches 124; Conservative 74; Mismatches 166; Indels 203; Gaps 26;

OY 77 VIVFVALIYMLGVSIADR-FMASIEVITSQEREVTIKKNGESTSTTTIRNMEVSN 135
 b 131 VVLHIFGMVYVALAIYDEYFVALGVTEK-----LQI-SEDAVG 172
 OY 136 LTLMASSAPRILSLIEVCGHFLA-GDLPSTIVGSAANMFLITICVYVPDGET 194
 Db 173 AFPMAGSAPRLFTSLIGV-----FISHNMGIGTIVGAVENILFVIGTCLF-----S 223
 OY 195 RKIKHARFEITAAASIFAYILY-----MILAVSPGVYVMEGLTFEPVCV----- 245
 Db 224 RRLILH-----TWWPLRDISFYVDLMLLFLFDSYIDMWESILLITAYATVFTMK 277
 OY 246 ---LLAVVADK-----RLLFYKYMKKYRTDKHNGIIEFGDHKGIEMDKMM- 292
 Db 278 HNVSLQWVKELSKKLNAVQAASAEHMRK-----SSVAVAEQGTFR-----ADCKKLQ 327
 OY 293 -----NS-----HFLDGNLVPLEKGEVDSRRMILILADLAK 326
 Db 328 PTTALQRTSSASLHNSQMRSTIFQMLHTLD-----PLAGAF-----KRVILSLIAEV 379
 OY 327 HPEKDLQLEVANYALSHQOKSRAFYRIQATRMWTGAGNLTIKHAAQKASSMSV 386
 Db 380 KADS-----LTGGT-----KPEAEENQASQ----- 401
 OY 387 HTDEPDLISKYFDPSCSYQLENCGAVLLTVRRKGGDKMTYVDYKTEDSANAGADY 446
 Db 402 -----NTQVMPAS-----DSEPSKQKQEDTPQDQOPSD- 434
 OY 447 EFTGTVLAKPGETOKEPSVGIIDDIPEDEHFFVRLSNVLEEQPEEGPRAFNEL 506
 b 435 -----NSESSSSSEDDSDDDSTDEE-----NDEPLSLEWPTRRKQAIYFL 478
 OY 507 PLPRAVLASPCVAVYTIIL---DDHAGITFECDRI-----HYSESIGVME 549
 Db 479 -FP---IYFPLMSTIPDVANPDSKKEFYITTFGSIITWIAFSYLMVMAHVGERTIGISE 534
 OY 550 VKVLRSGARGTIVFPRTVEGTANGG 576
 Db 535 EIMGLTIIAAGTSIPDLITSVIAVRKG 561

RESULT 13
 NKX2_HUMAN
 ID NKX2_HUMAN STANDARD; PRT; 661 AA.
 AC O9U140; O9NZ04; O9NTN5;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium/potassium/calcium exchanger 2 precursor (Na(+)/K(+)/Ca(2+)-
 GN exchange protein 2) (Retinal cone Na-Ca+K exchanger).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE-Retina;
 RX MEDLINE=20130359; PubMed=10662833;
 RA Prinsen C.F.M., Szerencsei R.T., Schnetkamp P.P.M.;
 RT "Molecular cloning and functional expression of the potassium-
 RT dependent sodium-calcium exchanger from human and chicken retinal cone
 RT photoreceptors.";
 RL J. Neurosci. 20:1424-1434(2000).
 RN [2]
 RP SEQUENCE OF 311-376 FROM N.A. (ISOFORM 1).
 RA Sutra H.;
 RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Critical component of the visual transduction cascade,
 CC controlling the calcium concentration of outer segments during
 CC light and darkness. Light causes a rapid lowering of cytosolic
 CC free calcium in the outer segment of both retinal rod and cone
 CC photoreceptors and the light-induced lowering of calcium is caused
 CC by extrusion via this protein which plays a key role in the
 CC process of light adaptation. Transports one Ca(2+) and one K(+) in
 CC exchange for four Na(+).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
 CC -----
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 CC -----

DR EMBL: AF097366; AAF21810.1; -;
 DR EMBL: AF177987; AAF25811.1; -;
 DR EMBL: AL133281; CAB92751.2; -;
 DR Genew: HGNC:10976; SLC24A2.
 DR InterPro: IPR004481; K_NaCaexchg.
 DR InterPro: IPR004837; NaCa_Exmemb.
 DR Pfam: PF01699; Na_Ca_Ex.3.
 DR TIGRFAMS: TIGR00367; K_NaCaexchang-rel.1.
 KW Vision; Transport; Antiport; Symport; Calcium transport;
 KW Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
 KW Signal; Repeat; Alternative splicing.
 FT SIGNAL 1 58
 FT CHAIN 59 661
 FT DOMAIN 59 132 SODIUM/POTASSIUM/CALCIUM EXCHANGER 2.
 FT TRANSMEM 133 153 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 154 178 POTENTIAL.
 FT TRANSMEM 179 199 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 200 204 POTENTIAL.
 FT TRANSMEM 205 225 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 226 243 POTENTIAL.
 FT TRANSMEM 244 264 POTENTIAL.
 FT DOMAIN 265 286 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 287 469 POTENTIAL.
 FT DOMAIN 470 490 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 491 497 POTENTIAL.
 FT DOMAIN 498 518 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 519 533 POTENTIAL.
 FT DOMAIN 534 554 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 555 569 POTENTIAL.
 FT DOMAIN 570 580 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 591 602 POTENTIAL.
 FT DOMAIN 603 623 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 624 630 POTENTIAL.
 FT DOMAIN 631 651 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 652 661 POTENTIAL.
 FT REPEAT 174 214 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 341 572 ALPHA-1.
 FT CARBOHYD 111 111 ALPHA-2.
 FT CARBOHYD 360 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 376 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 661 AA; 73663 MW; E6359C1F95C3AB3E CRC64;

Query Match	6.3%	Score 203.5;	DB 1;	Length 661;
Best Local Similarity	22.3%	Pred. No. 4.6e-07;		
Matches 128;	Conservative 91;	Mismatches 204;	Indels 151;	Gaps

28;

```

0Y 39 PSIONNESCSSGSSDCKEGVLTPIWPEBNP-SLGD-KIAVIYVFAVLIYMFGLGVSIAD 96
Db 101 PPLSNEGGS-ENSTDHOGD-----YKDFJSEERKGAIIHLVGMITMFIATLAVCD 154
QY 97 R-FMASIEVITSQREVIYIKKPNGETSTTIRVWNEVSNILTMALGSSAPEILSLIEV 155
Db 155 EFVPSLVTIEK-----LGI-SDVACATFMAAGSAPBELTSLIGV 196
QY 156 CGHGPIA-GDIPSTIVGSAFNNFIIGCVYVIPDGETRIKHLRVEFIYTAAMSIYAV 214
Db 197 ----FIASHNIGIGTIVGSAFNILFIYGMALF-----SREILNL-----TWMPLEFD 241
QY 215 IWL-----MLANFSQVYVWVWGLLT-FFPVYCL-----AWVADKRLPLPKYM 261
Db 242 VSFIVYDILMIIFLNLNIMWESSLLLTATFYCYVVEKKNVNOVEKW--KOMINRKV 299
QY 262 HKKRTOKHRIIIFETEGDHP-----KGIEMDGKMANSH-FLDGNLVPLEKREVEDSR 314
Db 300 VKYVAREQAKPSAARBDDEPTLPRAKRLDROGSSASLHNSLNRNSTFOL----- 349
QY 315 EMIRILDOKHBEKDLDOLEVANYALSHOOKSRAFYRIQATRMTCAGNIIKHA 374
Db 350 -MHTLDPLAE-----ELGSYGLKLYD-----TWMEGRPREKASI 385
QY 375 --EAKKASSMSVHTDEPF-----DFISKVFEPDPCSTOCLENGCAVLLTVYRKGDMS 426
Db 386 LHKIAKK-----KCHVENERONGANAHVKEILPNSTSDVETPSSDASEPVONGNLS 440
QY 427 KTMVYDKTEBDGSANAGADEVFETGTVVLKPGETOKESYGIITDOIIEEDHHPFVLSN 486
Db 441 HNT-----EGAAQIADAEEDOPLESJLAPSETRKQVTLIYFPIYF--LWITLPLD 489
QY 487 VRIEEOPEEGMPAIFNSLPPLPRAVLASPCVATVITLLDDHAGIFTECDTI---HVS 542
Db 490 VR--KPSRKFPPIYFGSI-----TWIANFVSLVWMMAHQV 555
QY 543 ESTGVMEVKVLTISGANGTVIVPRVYEGTAKGG 576
Db 526 ETIGISEIMGLTILAGTISIPDLITSVIYARKG 559

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RESULT 14	
NKX1_RAT	
ID	STANDARD; PRT; 1181 AA
NKX1_RAT	

15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Sox1un/pocass1un/calcium exchanger 1 precursor (Na⁺)/(K⁺)/Ca²⁺)-
exchange protein 1 (Retinal rod Na-Ca⁺ exchanger).
SLC24A1 OR NCKX1.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;

RP SEQUENCE FROM N.A.Y. AND ALTERNATIVE SPLICING.
RC STRAIN-Sprague-Dawley; TISSUE-Eye;
MEDLINE-20217335; Pubmed-10751311;
RA Poon S., Leach S., Li X.-F., Tucker J.E., Schnetkamp P.P.M.,
RA Lytton J.;
RA "alternatively spliced isoforms of the rat eye
RT sodium/calcium+potassium exchanger NCKX1.";
LT Am. J. Physiol. 278:C651-C660(2000).

RP SEQUENCE OF 1067-1155 FROM N.A.
RA White K.E., Gesek F.A., Friedman P.A.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases

CC	-I- FUNCTION:	Critical component of the visual transduction cascade,
CC		controlling the calcium concentration of outer segments during
CC		light and darkness. Light causes a rapid lowering of cytosolic
CC		free calcium in the outer segment of both retinal rod and cone
CC		photoreceptors and the light-induced lowering of calcium is caused
CC		by extrusion via this protein which plays a key role in the
CC		process of light adaptation. Transports one Ca(2+) and one K(++) in
CC		exchange for four Na(+).
CC	-I- SUBCELLULAR LOCATION:	Integral membrane protein.
CC	-I- ALTERNATIVE PRODUCTS:	4 isoforms; 1 (shown here) 2, 3 and 4; are
CC		produced by alternative splicing.
CC	-I- TISSUE SPECIFICITY:	Highly expressed in the eye.
CC	-I- SIMILARITY:	BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC		-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb.ch/announce/	
CC	or send an email to license@isb-slb.ch).	
CC		-----
DR	EMBL:	A6716688; AAD53121.1; -
DR	InterPro:	IIPR004817; K_NacCaexchang.
DR	InterPro:	IIPR004481; K_NacCaexchng.
DR	Famfam:	PF01699; Na_Ca_Ex_3.
DR	TIGRFAMs:	TIGR00367; K_NacCaexhang-rel; 1.
DR	TIGRFAMs:	TIGR00927; 2A1904; 1.
KW	Vision;	Transpot; Antiport; Symport; Calcium transport;
KW	Transmembran;	Glycoprotein; Phosphorylation; Signal; Repeat;
KW	Alternative splicing.	
FT	SIGNAL	1..38
FT	CHAIN	39..1181
FT	DOMAIN	39..419
FT	TRANSMEM	420..440
FT	DOMAIN	441..464
FT	TRANSMEM	465..485
FT	DOMAIN	486..491
FT	TRANSMEM	492..512
FT	DOMAIN	513..519
FT	TRANSMEM	520..544
FT	DOMAIN	545..552
FT	TRANSMEM	553..569
FT	DOMAIN	570..989
FT	TRANSMEM	990..1010
FT	DOMAIN	1011..1017
FT	TRANSMEM	1018..1038
FT	DOMAIN	1039..1053
FT	TRANSMEM	1054..1074
FT	DOMAIN	1075..1092
FT	TRANSMEM	1093..1123
FT	DOMAIN	1114..1121
FT	TRANSMEM	1122..1142
FT	DOMAIN	1143..1150
FT	TRANSMEM	1151..1171
FT	DOMAIN	1172..1181
FT	REPEAT	461..501
FT	REPEAT	1061..1092
FT	DOMAIN	730..905
FT	REPEAT	741..741
FT	REPEAT	742..754
FT	REPEAT	755..766
FT	REPEAT	767..778
FT	REPEAT	779..791
FT	REPEAT	792..804
FT	REPEAT	805..817
FT	REPEAT	818..830
FT	REPEAT	831..843
FT	REPEAT	844..856
FT	REPEAT	857..869
FT	REPEAT	870..881

RN	[1]	
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).	
RC	STRAIN-Sprague-Dawley; TISSUE-Brain cortex;	
RX	MEDLINE=96129830; PubMed=9461611;	
RA	Ts'oi M., Rhee K.-H., Bungard D., Li X.-F., Lee S.-T., Auer R.N.,	
RT	Lytton J.:	
RT	"Molecular cloning of a novel potassium-dependent sodium-calcium	
RL	exchanger from rat brain."	
CC	J. Biol. Chem. 273:4155-4162(1998).	
CC	-1- FUNCTION: Critical component of the visual transduction cascade,	
CC	controlling the calcium concentration of outer segments during	
CC	light and darkness. Light causes a rapid lowering of cytosolic	
CC	free calcium in the outer segment of both retinal rod and cone	
CC	photoreceptors and the light-induced lowering of calcium is caused	
CC	by extrusion via this protein which plays a key role in the	
CC	process of light adaptation. Transports one Ca(2+) and one K(+) in	
CC	exchange for four Na(+).	
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.	
CC	-1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are	
CC	produced by alternative splicing.	
CC	-1- TISSUE SPECIFICITY: Expressed abundantly in all regions of the	
CC	brain and weakly in the eye, large intestine and adrenal tissue.	
CC	-1- SIMILARITY: BELONGS TO THE SLIC2A4 FAMILY OF TRANSPORTERS.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; AF021923; AACI9405.1; -	
DR	EMBL; AF027506; AACI9404.1; -	
DR	InterPro; IPR004481; K_NacCaexchng.	
DR	InterPro; IPR004837; NaCa_Extmbd.	
DR	Pfam; PF01699; Na-Ca_Ex; 2.	
KW	TIGRFAMs; TIGR00357; K_NacCaexchang-rel; 1.	
KW	Vision; Transport; Antiport; Symport; Calcium transport;	
KW	Potassium transport; Sodium transport; Transmembrane; Glycoprotein;	
KV	Signal; Repeat; Alternative splicing.	
FT	SIGNAL	1 58
FT	CHAIN	59 670
FT	DOMAIN	59 133
FT	TRANSMEM	134 154
FT	DOMAIN	155 179
FT	TRANSMEM	180 200
FT	DOMAIN	201 205
FT	TRANSMEM	206 226
FT	DOMAIN	227 244
FT	TRANSMEM	245 265
FT	DOMAIN	266 266
FT	TRANSMEM	267 287
FT	DOMAIN	288 478
FT	TRANSMEM	479 499
FT	DOMAIN	500 506
FT	TRANSMEM	507 527
FT	DOMAIN	528 542
FT	TRANSMEM	543 563
FT	DOMAIN	564 578
FT	TRANSMEM	579 599
FT	DOMAIN	600 611
FT	TRANSMEM	612 632
FT	DOMAIN	633 639
FT	TRANSMEM	640 660
FT	DOMAIN	661 670
FT	REPEAT	175 215
FT	REPEAT	550 581
FT	CARBOHYD	112 112
FT	VARSPLIT	360 376
FT	CONFLICT	309 309
SO	SEQUENCE	670 AA; 74656 MW; 4E855A467FC6679E CRC64;

